

FIGURE 1

CGGACGCGTGCGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC
TGTGCCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCCGGC
GTTTGGCCCCAGGACGGGGCCCATGTGGTCGTCAGCAGCCGGAAGCAGCAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTCAACCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAACAGCCTTGCTGGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAAGTGCCTAGCACCTGGACTTATCAA
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCTGTGCTCT
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT
CTGAGGACCGGGAGACAGCCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCTCTGC
ATTCACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTTGCT
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT
GAGTCTACCTTGGCAAAGACCAAGATATTTTTCTCTGGGCCACTGGTGAATCTGAGGGGTGA
TGGGAGAGAAGGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

Variable	Mean	SD	Min	Max
Age	38.5	12.5	18	65
Gender	Male	Female		
Marital status	Married	Single		
Education	High school	College		
Occupation	Manager	Worker		
Income	\$10,000	\$20,000		
Health status	Good	Poor		
Exercise frequency	Weekly	Monthly		
Stress level	Low	High		
Sleep quality	Good	Poor		
Dietary habits	Healthy	Unhealthy		
Alcohol consumption	None	Occasional		
Tobacco use	Non-smoker	Smoker		
Family size	2	3		
Work hours	40	50		
Commuting time	30	45		
Home ownership	Renter	Owner		
Neighborhood safety	Safe	Unsafe		
Access to green spaces	Yes	No		
Public transportation	Used	Not used		
Crime rate	Low	High		
Weather conditions	Good	Poor		
Local economy	Strong	Weak		
Community involvement	Active	Passive		
Local government	Effective	Ineffective		
Local culture	Diverse	Homogeneous		
Local history	Rich	Poor		
Local infrastructure	Good	Poor		
Local services	Good	Poor		
Local amenities	Good	Poor		
Local environment	Good	Poor		
Local quality of life	Good	Poor		
Local satisfaction	High	Low		
Local happiness	High	Low		
Local well-being	High	Low		
Local health	Good	Poor		
Local safety	High	Low		
Local security	High	Low		
Local peace	High	Low		
Local harmony	High	Low		
Local balance	High	Low		
Local stability	High	Low		
Local order	High	Low		
Local justice	High	Low		
Local equity	High	Low		
Local fairness	High	Low		
Local integrity	High	Low		
Local honesty	High	Low		
Local trust	High	Low		
Local respect	High	Low		
Local tolerance	High	Low		
Local compassion	High	Low		
Local kindness	High	Low		
Local generosity	High	Low		
Local helpfulness	High	Low		
Local cooperation	High	Low		
Local teamwork	High	Low		
Local collaboration	High	Low		
Local partnership	High	Low		
Local alliance	High	Low		
Local coalition	High	Low		
Local confederation	High	Low		
Local federation	High	Low		
Local union	High	Low		
Local association	High	Low		
Local organization	High	Low		
Local institution	High	Low		
Local establishment	High	Low		
Local system	High	Low		
Local structure	High	Low		
Local framework	High	Low		
Local foundation	High	Low		
Local base	High	Low		
Local core	High	Low		
Local center	High	Low		
Local hub	High	Low		
Local node	High	Low		
Local point	High	Low		
Local spot	High	Low		
Local site	High	Low		
Local place	High	Low		
Local area	High	Low		
Local region	High	Low		
Local territory	High	Low		
Local domain	High	Low		
Local jurisdiction	High	Low		
Local authority	High	Low		
Local power	High	Low		
Local influence	High	Low		
Local impact	High	Low		
Local effect	High	Low		
Local result	High	Low		
Local outcome	High	Low		
Local consequence	High	Low		
Local effectuation	High	Low		
Local causation	High	Low		
Local production	High	Low		
Local generation	High	Low		
Local creation	High	Low		
Local development	High	Low		
Local growth	High	Low		
Local expansion	High	Low		
Local increase				

><MW: 29537, pI: 8.97, NX(S/T): 1

amino acids 276-278

FIGURE 3

GCGCCCTGAGCTCCGCCTCCGGGCCCCGATAGCGGCATCGAGAGCGCCTCCGTGAGGACCAGGCGGCG
CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCTGCAGAACCAGGTGGC
GCGGCTGGAGGAGGAGAACCGAGACTTTCTGGCTGCGCTGGAGGACGCCATGGAGCAGTACAACTGC
AGAGCGACCGGCTGCGTGAGCAGCAGGAGGAGATGGTGGAACTGCGGCTGCGGTTAGAGCTGGTGCGG
CCAGGCTGGGGGGGCTGCGGCTCCTGAATGGCCTGCCCTCCCGGTCCTTTGTGCCTCGACCTCATAC
AGCCCCCTGGGGGGTGCCACGCCCATGTGCTGGGCATGGTGCCGCCTGCCTGCCCTCCCTGGAGATG
AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT
GAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGCCGCC
CAGGCGGACCTTACACCTGCGCAGAAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGGCACGCCAG
GGAGTCTGCCAGAGAGGAAGGGCCAGAGCTTTGCCTTGAGGAGTTGGATGCAGCCATTCCAGGGTCC
AGAGCAGTTGGTGGGAGCAAGGCCCGAGTTCAGGCCCGCCAGGTCCCCCTGCCACAGCCTCAGAGTG
GCGGCTGGCCCAGGCCAGCAGAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA
TTGGCGAGCTGGTCCGCACAGGAAAGGCAGCTCAGGCCCTGAACCGCCAGCACAGCCAGCGTATCCGG
GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCAGCTGCGGGAGCT
CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTTCCGCAGGAGGGTCTGTG
CGGGCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTGTCACTGTCTG
GCCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGAGGGACA
GCTGCAGAGGCGGCTTCGCGAGGAGACGGAGCAGAAGCGGCGCCTGGAGGCAGAAATGAGCAAGCGGC
AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATTAAGACGGAA
GAGATCGCGGCCTTCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTCAGCCTGGAACAGCA
GCAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAGCGGCGGG
CGCTGGAGGAGCTGGGGGAGGAGCTCCACAAGCGGGAGGCCATCCTGGCCAAGAAGGAGGCCCTGATG
CAGGAGAAGACGGGGCTGGAGAGCAAGCGCCTGAGATCCAGCCAGGCCCTCAACGAGGACATCGTGCG
AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGCTGCGGCAGGGCA
GCGCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGCTGCTC
AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGGAGTCTGCTGTCCCCCGAGGAGGAGCGGAC
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA
CATGCCGCCAGCGGGTGCTTCGGGCCTCAGCCTCGTTGCTGTCCAGTGCGAGATGAACCTCATGGCC
AAGCTCAGCTACCTCTCATCCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTTGACAAGGTGGTGAC
GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCTTCTCGGAACCTGGAGATGCAGCTGGAGGAGCAGC
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCCTGGAGATGGACCGCCAGCTGACC
CTGCAGCAGAAGGAGCACGAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCGAGACCACCTCGGTGA
AGGGTTAGCAGACAGCAGGAGGCAGTATGAGGCCCGGATTCAAGCTCTGGAGAAGGAACTGGGCCGTT
ACATGTGGATAAACCAGGAACCTGAAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT
GGGGAGAAGAGGAGCCTGTGCTCGGAGGGCAGACAGGCTCCTGGAATGAAGATGAGCTCCACCTGGC
ACCCGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGACGCGGGACT
TGGTCCACGCTCCGTTACCCTTGACCTGGAAACGCTCGAGCCTGTGTGGTGAGGAGCAGGGGTCCCC
GAGGAACCTGAGGCAGCGGGAGGCGGCTGAGCCCCTGGTGGGGCGGGTGCTTCCTGTGGGTGAGGCAGG
CCTGCCCTGGAACCTTGGGCCTTTGTCCAAGCCCCGGCGGGAACCTGCGACGAGCCAGCCGGGGATGA
TTGATGTCCGGAATAAACCCTGTAAAGCCCTCGGGGCAGACCCTGCCTTGAGGGGAGACTCCGAGCCT
GCTGAAAGGGGCAGCTGCCTGTTTTGCTTCTGTGAAGGGCAGTCCTTACCGCACACCCTAAATCCAGG
CCCTCATCTGTACCCTCACTGGGATCAACAAATTTGGGCCATGGCCAAAAGAACTGGACCCTCATTT
AACAAAATAATATGCAAATTTCCACCACCTTACTTCCATGAAGCTGTGGTACCCAATTGCCGCCTTGTG
TCTTGCTCGAATCTCAGGACAATTCTGGTTTTAGGCGTAAATGGATGTGCTTGTAGTTTACGGGTTTG
GCCAAGAATCATCACGAAAGGTGCGTGGCAACCAGGTTGTGGTTTAAATGGTCTTATGTATATAGGG
GAAACTGGGAGACTTTAGGATCTTAAAAAACCATTTAATAAAAAAAATCTTTGAAGGGAC

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLQSDRLREQQEEMVELRLRLLELVRPGWGGLRLLNGLPPGSFVPRPHTAPLGGAHAHV
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGSLPERKGPELCLEELDAAIPGSRAVGGSKARVQARQVPPATAS
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQVLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQQGQLQRRRLREETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQRKRSSGSGSVVSLEQQQKIEEQKKWLDQEMEKVLQORRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAAQSQQQIRGEIDS
LRQEKDSSLKQRLEIDGKLQGSLLSPEEERTLFLQLEAIEALDAAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSETRALLCKYFDKVVTLRREEQHQQQIAFSELEMQLEEQQR
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGHSGGEEKRSLCSEGRQAPGNEDELHLAPELLWLSPLTEG
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACCTTATCTCCCATCTCCCGGAGCTGTAC
CAGGAACAGGAGGCACGTCCTGTACCCATTAAAAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTCCAGCTCCCCCTTCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCCACATTTACCATCT

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700

><subunit 1 of 1, 125 aa, 1 stop

><MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFLQCSKGTTDAPVGSGWLWCQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRSCTRNRRHVLYP

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

TO/222T"442222T

FIGURE 7

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT
TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG
AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCG
GAGAAGCGGGGACGAGGCCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCCG
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGG
TCGCCGGCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCGCTGCTACCCCTG
CGCCCGCTGCGAGCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG
GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCTCGGCCGCGCTCCCCGCCCGCCC
GCCCGCCGGGACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
GTTCCCTCCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG
AAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC
TGGGTCTCCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACAC
CCCGCAGGCGGAAGCCCTGGCCGAGCCGCCAGGACGCGATTGGCCCGGAACCTCGCGCCCA
CGCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCT
GTGCACCGAGGAGGGGCGGCTGTGCGCGCAGCCGAGTGCCCGAGGCTGCACCCGCGCTGCA
TCCACGTCGACACGAGCCAGTGCTGCCCCGAGTGCAAGGAGAGGAAGAATACTGCGAGTTC
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTGCTG
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGACGCGTGTCCCAGACGGAGTGTGTGGACC
CTGTGTACGAGCCTGATCAGTGCTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAA
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGACCATATGCCACTGTAC
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC
AAATGTAGACGCTTCCCAGAACACAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAA
CATTTAGATGACTCTGGGAACTATCAGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAA
TTGTTGGTACTTTTCTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTT
AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACAG
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG
CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTCAAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

><MW: 35296, pI: 5.37, NX(S/T): 0

MPSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL
GRPARDEGGSGRDWKSksGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPQAEALA
AAAQDAIGPELAPTPEPPEEYVYPDYRGKGCVDSESGFVYAIGKFAFGPSACPCLCTEEGPL
CAQPECPRLLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPECRCRCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEETWR
IERQAMCTRHECRQM

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCGTGCCAGGAGACCGGCAGTGTG
CTACCTGTGTGCAGCCCCCTTGGAACTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
GAGCATTGAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTTGGCCCTTCCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTATATCTACTCACCTAACAGCA
ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847

><subunit 1 of 1, 437 aa, 1 stop

><MW: 46363, pI: 6.22, NX(S/T): 3

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVCPSC

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTG
GCTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTTCTAGAGCCGAGGGACCCGGTG
CTCGTCGCTCAGCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT
TGTCGGGCCCCGAGGCTCCGTGGCGGGACCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG
CAGCTGGTCGCCCTCATTTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT
GAGGCAGCTGCACGGGTTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCG
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCT
CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGC
ACCGCTGCATGGATAGCAGCGCCGCCTTCTGCAGGGGCTGTGGCAGCACTACCACCCTGGC
TTGCCGCCGCCGGACGTGCGAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAAT
GAGATTTTTTTGATCACTGTGAGAAGTTTTTAACTGAAGTAGAAAAAATGCTACAGCTCTTT
ATCACGTGGAAGCCTTCAAACTGGACCAGAAATGCAGAACATTTTTAAAAAAGTTGCAGCT
ACTTTGCAAGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTTACCTG
TTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATG
ATGCAAAGGTATTAGAATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTAT
ACTATTAACAGTCGATCCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAAGC
AGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATG
CAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACA
GCGTACAATTACAAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGC
CTCGAACCTGATATTTGTGCTTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAATTCC
GAGTGCAGATGTTATTAAATGAAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCA
TTTTATGAAGATCTGAAGAACCCTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGA
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACTATGAGTAACTGAAGAACATTTTT
AATTCTTTAGGAATCTGCAATGAGTGATTACATGCTTGTAATAGGTAGGCAATTCCCTTGATT
ACAGGAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTC
TCTGGGTTTGGACATGAAATGTAAGAAAAGATTTTTCACTGGAGCAGCTCTCTTAAGGAGAA
ACAAATCTATTTAGAGAAACAGCTGGCCCTGCAAATGTTTACAGAAATGAAATTCTTCCTAC
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTTCATAATAACACTTGAAAAGTGCT
GGAGTAACAAAATATCTCAGTTGGACCATCCTTAACTTGATTGAACTGTCTAGGAACCTTAC
AGATTGTTCTGCAGTTCTCTCTTTCTCCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC
AGGAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT
TTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAA
TGAAAATAAATATTTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCCTT
TTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATATGTTTGGACAATTAGCAAC
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTTTCAATCTGT
CACTTGGCTTCGATTTTTTATATTTTCTTATTATATGAAATGTATCTTTTGGTTGTTTGATTT
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA
TAAAGAAAATTCTTGTGACTTTAAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLS
GPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAAGTGTCTTGCATCATTACGGATTTCG
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAGATGAACAAACCATATGTGTTTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATCTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACCGATT
CCAGAGCCAATCCCAGATTTTCGCAATTCTTCTTTCCACTTAAACTCTGAAAACAGGCACCTTTGGTGTTCCTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATGGGGGGGTTCTGGTTFGTCCTTGCTGTACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAACAGATGGAGTTAACTACATCCGCACGTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACCTCGGACAGAGCTAGACACTCATTAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTAATCTGTTTCTGGCCTGATTCCTCGCATGAGTATTAGG
GTGATCTTAAAGAGTTTGCTCAGTAAACGCCCCGTGTGGGCCCTGTGAAGCCAGCATGTTCAACCACTGGTCGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCCGCGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCCTGAGGAACCCGTGTTGTCCAACAGGGTGTGAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAAGAGTATTTTACCACAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTCT
CACACAAGTTTTAGCCTTTTTTACAAGGGAACCTCATCTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAAATCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCCGCTCTAGCTCACTGTTGCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAATTATTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT
CCCCTGTTTCTTGTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAAGCTCAGGTGGAGCAGCCAGGTGAAAGGCCCTGGCGGGGAGGAAAG
TGAAACGCCTGAATCAAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTTCATCCGCCGAGACACTGCTCCCAT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA
GAATGGCTCTCACTACTACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCGCTTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT
TCTTGGTTGTCTAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACCTTTACACTAGTGCCA
TGGGAACAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTTGTTTAAAC
CTCATTTATAAAAGCTTCAAAAAACCCA

[illegible]

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><subunit 1 of 1, 310 aa, 1 stop
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MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGG
VLVVLAVLALITLGICCAYYRRGYFINNKODGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Signal peptide:

amino acids 1-30

amino acids 243-263

amino acids 104-107, 192-195

amino acids 107-110

amino acids 106-109, 296-299

amino acids 69-77

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 15

CAGGACCAGGTCTTCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG
ATCCTGCTGACGCTGGGCCCCGCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTTCCGGAG
GAGAAGCCACTGCCCACCGCTTCTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCTGACTGGCTGAAGCTG
CGCATGATCCGTTCTGAGGTGCTCCGCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCAGCAGCTGCTGCTG
TTCGTGCAGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACCTCCTCCAGTTCTTGGACCAGGCAGTGGCCCCAC
GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCCACCTGGTGGAGGTCCAGCATGAGCGC
GGCGCTCCGGAGGCCAGACTTTCACCTCCTTGCTCACAGCCTCCCTGCCGCCCGCCGAGACAGCACAGAGGCA
CCCAAACCAAAGAGCAGCCCAGAGCAGCCCATAGGCCAGGGCCGGATTTCGGGTGGGGACCCAGCTCCGGGTGCTG
GGCCCTGAGGACGACCTGGCTGGCATGTTCTCCAGATTTTCCCGCTCAGCCCCGACCCTCGGTGGCAGAGCTCC
AGTCCCCGCCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCCGCTGCTCCAGGGCAGCCCC
GAGGTGCCGGGCATCACGGTGCCTGCTGCAGGCCCTCGCCACCCTGCTCAGCTCCCCACACGGCGGTGCCCTG
GTGATGTCCATGCACCGTAGCCACTTCTGGCCTGCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCGCTGTGTG
CCACAGGACACCGGCTTCTCCTCGCTCTTCTGAAGGTGCTCCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC
GTGGAGGGCGGGCCCCCTGCCGGCACAGCTCAGGATGCTTGCCAGCCAGGCCCTCAGCCGGGCGCAGGCTCAGTGAT
GTGCGAGGGGGGCTCCTGCGCCTGGCCGAGGCCCTGGCCTTCCGTGAGGACCTGGAGGTGGTCAGCTCCACCGTC
CGTGCCGTCATCGCCACCCTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCCGGACCTGATCAGCAAAGTCTCTCCAG
GGGCTGATCAGAGGTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTTCTCTGCCACTGCGGATGCTGCC
TCCCCGTTTCCAGCCTGTAAGCCCGTTGTGGTGGTGAGCTCCCTGCTGCTGCAGGAGGAGGAGCCCCCTGGCTGGG
GGGAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGTGGGGCCCTCGTCAGGCCTCCTAGTGGAAGTGG
CTGGAATGCTGGACCCCGAGGTGGTCAGCAGCTGCCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGAGGAAG
GGCAAAGTTCAGGCCAGGTGCCCTCGTTCCGTCCCTACCTCCTGACCCTCTTACGCATCAGTCCAGCTGGCCC
ACACTGCACAGTGCATCCGAGTCTGCTGGGCAAGAGCCGGGAACAGAGGTTGACCCCTCTGCCTCTCTGGAC
TTCCTCTGGGCTGCATCCATGTTCTCGCATCTGGCAGGGGCGGGACCAGCGCACCCCGCAGAAGCGGCGGGAG
GAGCTGGTGTGCTGCGGTCCAGGGCCCGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCG
AGCCAGGACGGGGACACAGCCGCCCTGCAGCCTCATCCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG
GACGATGAGAGTGTGAGGAAGGTGACGGAGCACCTGTGAGGCTGCATCCAGCAGTGGGGAGACAGCGTGTGGGA
AGGCGCTGCCGAGACCTTCTCCTGCAGCTCTACCTACAGCGGCCGGAGCTGCGGGTGCCCGTGCCTGAGGTCTTA
CTGCACAGCGAAGGGGCTGCCAGCAGCAGCGTCTGCAAGCTGGACGGACTCATCCACCGCTTCATCACGCTCCTT
GCGGACACCAGCGACTCCCGGGCGTTGGAGAACCAGGGGGCGGATGCCAGCATGGCCTGCCGGAAGCTGGCGGTG
GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCCTGCACGGCCGCACCCACCTCAACTTC
CAGGAGTTCGGGCAGCAGAACCACCTGAGCTGCTTCTGACGTGCTGGGCTGCTGGAGCTGCTGCAGCCGCAC
GTGTTCCGCAGCGAGCACCAGGGGGCGCTGTGGGACTGCCTTCTGTCTTCATCCGCTGCTGCTGAATTACAGG
AAGTCTCTCCGCCATCTGGCTGCCTTCATCAACAAGTTTGTGCAGTTCATCCATAAGTACATTACCTACAATGCC
CCAGCAGCCATCTCCTTCTGCAAGACGCGGACCCGCTCCACGACCTGTCTTCGACAACAGTGACCTGGTG
ATGCTGAAATCCCTCCTTGCAGGGCTCAGCCTGCCAGCAGGGACGACAGGACCGACCGAGGCCCTGGACGAAGAG
GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGCCCCCTGGTCAGCGTCTCCCTGTTCACCCCTCTGACCGCGGCCGAG
ATGGCCCCCTACATGAAACGGCTTTCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
GAGATGTCCCGGCGGAGACCCGAGATCCTGAGCTTCTTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG
GAGTGTGCGCAACCTCGCCTTACAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTTC
CTGCCACGTTTCATGTACTGCCTGGGCAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCTGAG
TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTCCACCGGCCCTCCTGGTGGGCATGTACGGCCAGATG
GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATGTGAGCCCTGTGGCAGCCGA
CCCCCTCCAAGCCCCGGGCTCCCGTCCCCGGGGATCCTCGAGGCAAAGCCCAGGAAGCGTGGGCGTTGCTGG
TCTGTCCGAGGAGGTGAGGGCGCGAGCCCTGAGGCCAGGCAGGCCAGGAGCAATACTCCGAGCCCTGGGGTGG
CTCCGGGCGGCCGCTGGCATCAGGGGCCGTCCAGCAAGCCCTCATTCACCTTCTGGGCCACAGCCCTGCCGCGG
AGCGGCGGATCCCCCGGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAACTGTCAA

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRM
IRSEVLRLVDAALQDLEPQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY
MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLLSSPHGGALVMSMHRSHFLACPLLRLQLCQYQRCVPQDTGFSSFLKVLQMLQWLDS PG
VEGGPLRAQLRMLASQASAGRRLSDV RGGLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASFPACKPVVVVSSLLLQEEEEPLA
GGKPGADGGSLEAVRLGPSSGLLVDWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR
PYLLTLFTHQSSWPTLHQ CIRVLLGKSREQRFDPASLDFLWACIHVPRIWQGRDQ RTPQKR
REELVLRVQGPELISLVELILAEAETRSQDGD TAACSLIQARLP LLLSCCGDDESVRKVTE
HLSGCIQQWGDSVLGRRCRDLLQLYLQRP ELRVPVPEVLLHSEGAASSSVCKLDGLIHRFI
TLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLP MIAALLHGRTHLNFQEF RQQNHL
SCFLHVLG LLELLQPHVFRSEHQ GALWDCLLSFIRLLLNYRKSSRH LAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDL SFDNSDLV MLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSD IDEMSRRRPEILSFFSTNLQRL
MSSAECCRNLA FSLALRSMQNSPSIAA AFLPTFMYCLGSQDFEVVQTALRNLP EYALLCQE
HAAVLLHRAFLVGMYGMDPSAQISEALRILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 17

CCGGGCCATGCAGCCTCGGCCCCGCGGGCGCCCGCCGCGCACCCGAGGAGATGAGGCTCCGC
AATGGCACCTTCTTGACGCTGCTGCTCTTCTGCTGTGCGCCTTCCTCTCGCTGTCCTGGTA
CGCGGCACTCAGCGGCCAGAAAGGCGACGTTGTGGACGTTTACCAGCGGGAGTTCTTGCGC
TGCGCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG
GTGCTGGACGAGATCAAGAGGGCCGTGTGAGAAAGGCAGGCGCTGCGAGACGGAGACGGCAA
TCGCACCTGGGGCCGCCTAACAGAGGACCCCCGATTGAAGCCGTGGAACGGCTCACACCGGC
ACGTGCTGCACCTGCCCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT
CTGCAGCCCCGCGGTGCGCGTGGGCCAGGGCCGCACCGGAGTGTGCGGTGGTGATGGGCATCCC
GAGCGTGCGGCGGAGGTGCACTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGC
TGAGCCCCGAGGAGAAGGAGGACTCGGTTCATCGTGGTGCTGATCGCCGAGACTGACTCACAG
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCCCCACGGAGATCCATTCTGGGCT
CCTGGAGGTTCATCTACCCCTCCCCCACTTCTACCCTGACTTCTCCCGCCTCCGAGAGTCCT
TTGGGGACCCCAAGGAGAGAGTCAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCCTC
ATGATGTACGCGCAGTCCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA
GCCCAACTACCTGAGCACCATGAAGAACTTTGCACTGCAGCAGCCTTCAGAGGACTGGATGA
TCCTGGAGTTCTCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG
ATTGTAGAGTTCATTCTCATGTTCTACCGGGACAAGCCCATCGACTGGCTCCTGGACCATAT
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA
ACCTGCGGATCCGCTTCAAACCGTCCCTCTTCCAGCACGTGGGCACTCACTCCTCGCTGGCT
GGCAAGATCCAGAACTGAAGGACAAAGACTTTGGAAAGCAGGCGCTGCGGAAGGAGCATGT
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATAACCAGCACTTCACCCTGGAGAAAG
CCTACCTGCGCGAGGACTTCTTCTGGGCCTTCACCCCTGCCGCGGGGGACTTCATCCGCTTC
CGCTTCTTCCAACCTCTAAGACTGGAGCGGTCTTCTTCCGCAGTGGGAACATCGAGACCCC
GGAGGACAAGCTCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAACCCTCAGTCAGACA
AGGAGGCCCTGCAGGAGGGCCGCACCGCCACCCTCCGGTACCCTCGGAGCCCCGACGGCTAC
CTCCAGATCGGCTCCTTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTTCGGCCC
TCTGGAAGCACTGCGCCTCTCGATCCAGACGGACTCCCCTGTGTGGGTGATTCTGAGCGAGA
TCTTCCTGAAAAAGGCCGACTTAAGCTGCGGGCTTCTGAGGGTACCCTGTGGCCAGCCCTGAA
GCCCACATTTCTGGGGGTGTGCTCACTGCCGTCCCCGGAGGGCCAGATACGGCCCCGCCCAA
AGGGTTCTGCCTGGCGTGGGGCTTGGGCCGGCCTGGGGTCCGCCGCTGGCCCCGAGGGCCCTA
GGAGCTGGTGCTGCCCCCGCCCGCGGGCCGCGGAGGAGGCAGGCGGCCCCCACACTGTGCC
TGAGGCCCGGAACCGTTCGCACCCGGCCTGCCCCAGTCAGGCCGTTTTAGAAGAGCTTTTAC
TTGGGCGCCCCCGCTCTCTGGCGCGAACACTGGAATGCATATACTACTTTATGTGCTGTGTT
TTTTATTCTTGATACATTTGATTTTTTTCACGTAAGTCCACATATACTTCTATAAGAGCGTG
ACTTGTAATAAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLLLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDLRHAAEQESLKRSK
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGQGRGTGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVVRWRTKQNLD
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGT
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGD
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515